

002007 2224360

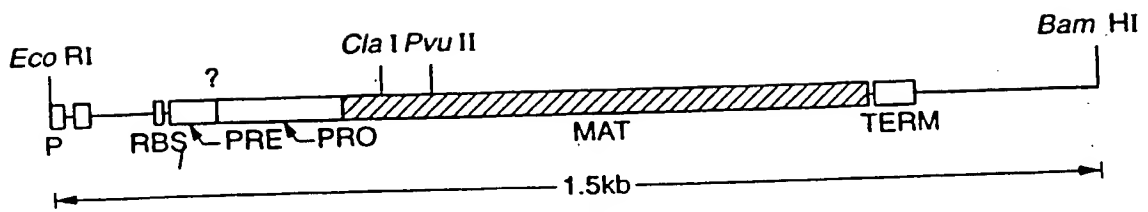


FIG. 1A

34 total
sheets

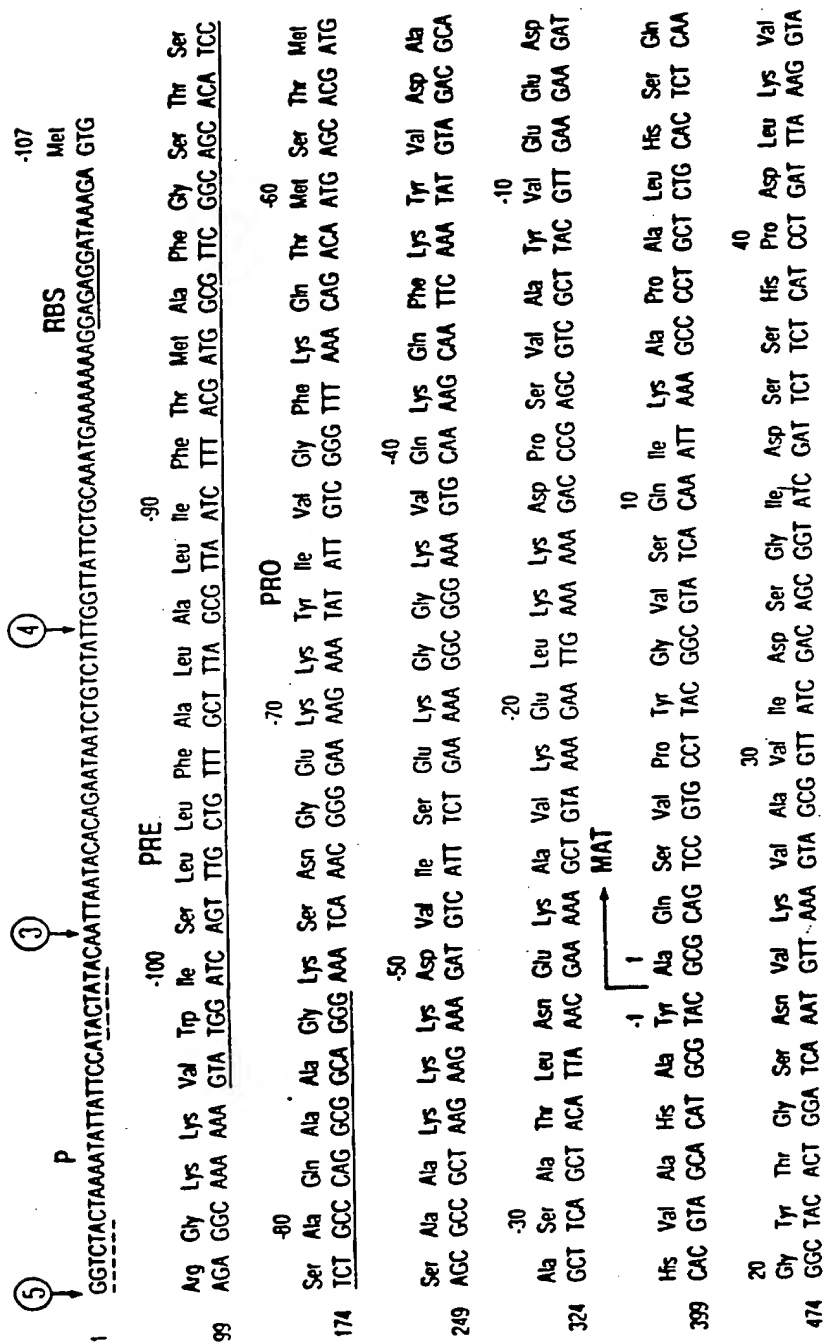


FIG. 1B - 1

549	Ala	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Asn	Asp	60	Asp	Ser	His	Gly	Thr	His	Val	Ala		
	GCA	GGC	GGA	GGC	AGC	ATG	GTT	CCT	TCT	TCT	GAA	ACA	AAT	CCT	TTC	CAA	GAC	AAC	AAC	TCT	CAC	GGA	ACT	CAC	GTT	GCC
70	Gly	Thr	Val	Ala	Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	Ala	Ser	Ala	90	Ser	Ala	Val	Lys
224	GGC	ACA	GTT	GGC	GCT	CTT	AAT	AAC	TCA	ATC	GGT	GTA	TTA	GGC	GTT	GGC	CCA	AGC	GCA	TCA	CTT	TAC	Tyr	Ala	Val	Lys
699	Val	Leu	Gly	Ala	Asp	Gly	Ser	Gly	Gln	Tyr	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ala	Asn	Asn	Met	
	GTT	CTC	GGT	GCT	GAC	GGT	TCC	GGC	CAA	TAC	AGC	TGG	ATC	ATT	AAC	GGA	ATC	GAG	TGG	GCG	ATC	GCA	AAC	AAT	ATG	
120	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Ala	Leu	Lys	Ala	Val	Ala	Val	Ala	Val	Val	Ala	
	GAC	GTT	ATT	AAC	ATG	AGC	CTC	GGC	GGA	CCT	TCT	GGT	TCT	GCT	GCT	TTC	AAA	GCG	GCA	GTT	GAT	AAA	GCC	GTT	GCA	
849	Ser	Gly	Val	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser	Thr	Val	Gly	Tyr	Pro	Gly	
	TCC	GGC	GTC	GTA	GTC	GTT	GGC	GCA	GGC	GGT	AAC	GAA	GGC	ACT	TCC	GGC	AGC	TCA	AGC	ACA	GTG	GGC	TAC	CCT	GGT	
170	Lys	Tyr	Pro	Ser	Val	Ile	Ala	Val	Gly	Ala	Val	Asp	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Val	Gly	Pro	
	AAA	TAC	CCT	TCT	GTC	ATT	GCA	GTA	GGC	GCT	GTT	GAC	AGC	AGC	AAC	CAA	AGA	GCA	TCT	TTC	TCA	AGC	GTA	GGA	CCT	
924	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Pro	Gly	Asn	Lys	Tyr	Gly	Ala	Tyr	Asn	Gly	
	GAG	CTT	GAT	GTC	ATG	GCA	CCT	GGC	GTA	TCT	ATC	CAA	AGC	ACG	CTT	CCT	GGA	AAC	AAA	TAC	GGG	GCG	TAC	AAC	GGT	
200	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His	Pro	Asn	Trp	Thr	Asn	Thr	
	ACG	TCA	ATG	GCA	TCT	CCG	CAC	GTT	GCC	GGA	GGG	GCT	GCT	TTC	ATT	CTT	TCT	AAG	CAC	CCG	AAC	TGG	ACA	AAC	ACT	
1074	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His	Pro	Asn	Trp	Thr	Asn	Thr	
	ACG	TCA	ATG	GCA	TCT	CCG	CAC	GTT	GCC	GGA	GGG	GCT	GCT	TTC	ATT	CTT	TCT	AAG	CAC	CCG	AAC	TGG	ACA	AAC	ACT	

FIG. 1B - 2

00200T"2344960

250 Gln
Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn
1149 CAA GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA CTT GGT GAT TCT TTC TAC TAT GGA AAA GGG CTG ATC AAC
270
Val Gln Ala Ala Ala Gln OC
1224 GTA CAG GCG GCA GCT CAG TAA AACATAAAACCGGCCCTGGCCCCCGCGGGTITTTTCTCTCCGCGCATGTTCAATCGCGTCC

TERM

1316 ATAATCAGCGATGGCTCCCTCTGAAATTTTAAACGAGAAACGGCGGGTTGACCCGGCTCAGTCCGTAACGGCCAAGTCTCTGAACGGTCTCAATCGCGG

1416 CTCCCCGGTTCCGGTCAGCTCAATGCCGTACGGTCGGGGGGTTTCTCTGATACCGGGGAGACGGCATTCGTAATCGGATC

FIG._1B - 3

FIG._1B - 1
FIG._1B - 2
FIG._1B - 3

FIG._1B

FIG. 2

COMPARISON OF SUBTILISIN SEQUENCES FROM:

B. amyloquelaciens
B. subtilis
B. ficheniformis
B. lentus

01	10	20	30	
A Q S V P Y G V S Q I K A P A L H S Q Q G Y T G S N V K V A V I D S G I D S S H P				
A Q S V P Y G I S Q I K A P A L H S Q Q G Y T G S N V K V A V I D S G I D S S H P				
A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P				
A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T * H P				
41	50	60	70	
D L K V A G G A S M V P S E T N P F Q D N N S H G T H V A G T V A A L N N S I G				
D L N V R G G A S F V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I G				
D L N V V G G A S F V A G E A Y N * T D G N G H G T H V A G T V A A L D N T T G				
D L N I R G G A S F V P G E * P S T Q D G N G H G T H V A G T I A A L N N S I G				
81	90	100	110	
V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D				
V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D				
V L G V A P S V S L Y A V K V L N S S G S G S Y S G I V S G I E W A T T N G M D				
V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N N G M H				
121	130	140	150	
V I N M S L G G P S G S A A L K A A V D K A V A S G V V V V A A A A G N E G T S G				
V I N M S L G G P T G S T A L K T V V D K A V S S G I V V A A A A A G N E G S S G				
V I N M S L G G A S G S T A M K Q A V D N A Y A R G V V V V A A A A G N S G N S G				
V A N L S L G S P S P S A T L E Q A V N S A T S R G V L V V A A S G N S G A G S				

FIG._3A

161
 SSSSTVGYPPGKYPSPVIAVGAVDSSNQRA SFS SSGPELDDVMA
 STSTVGYPPAKYPSTIAVGA VNSSNQRA SFS SSGSELEDDVMA
 STNTIGYPPAKYDSSVIAVGA VDNSSNQRA SFS SSGAELEDDVMA
 * * * I SYPARYANAMAVGATDQNNNRASFSQYGGAGLDIVA

201
 PGVSIQSTLPPGGNKYGAYNGTSMASPHVAGAAALILSKHHPN
 PGVSIQSTLPPGGTKYGAYNGTSMATPHVAGAAALILSKHHPN
 PGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHHPN
 PGVNVQSTYPPGSTYASLNGTSMATPHVAGAAALVKKKPNPS

241
 WTNNTQVRS SLENTTTKKLGGDSFY YGKGLIN VQAAQ
 WTNAAQVRRDRLESTATTYLGNSFFYYGKGLIN VQAAQ
 LSASQVRRNRRLSSSTATTYLGSSFFYYGKGLIN VQAAQ
 WSNVQIRRNHLLKNTATSLGSS TNL YGSLVNAEATR

FIG..3B

FIG..3



0067822 40200

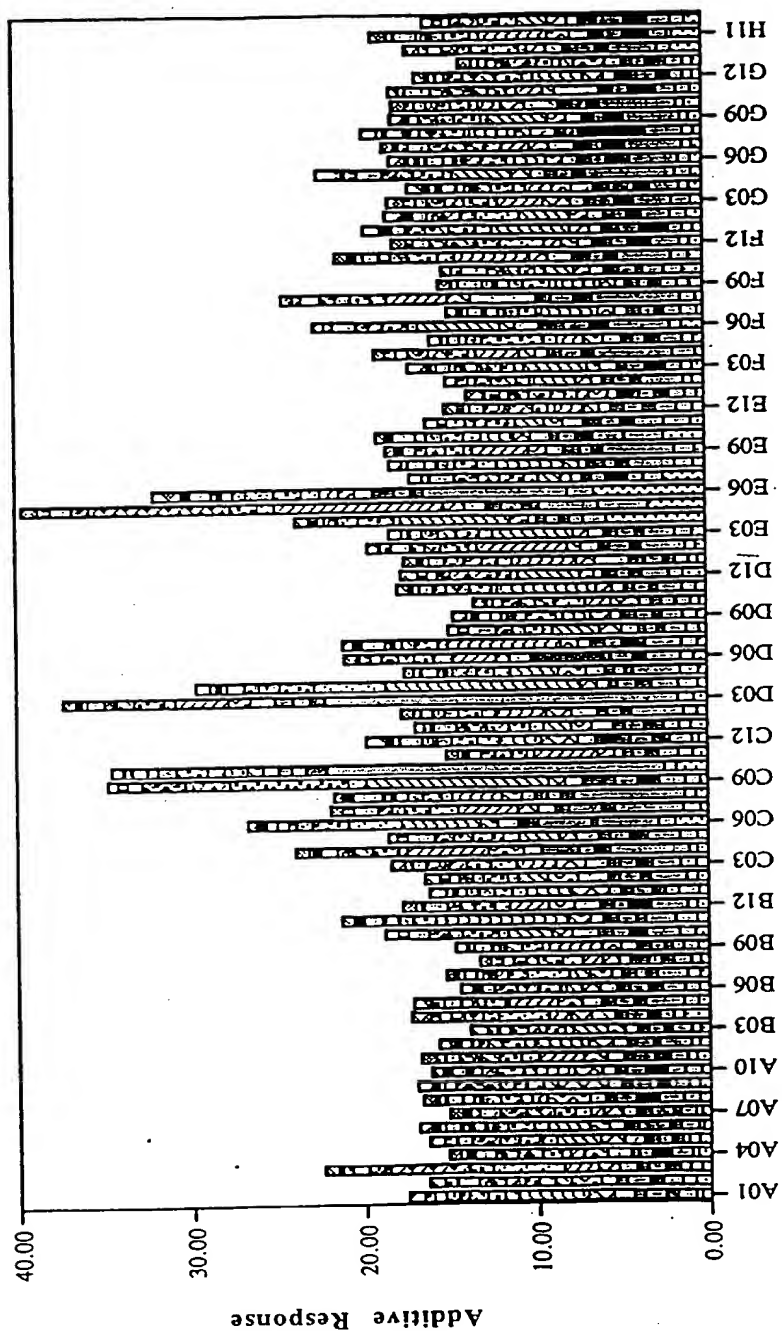


FIG. 4

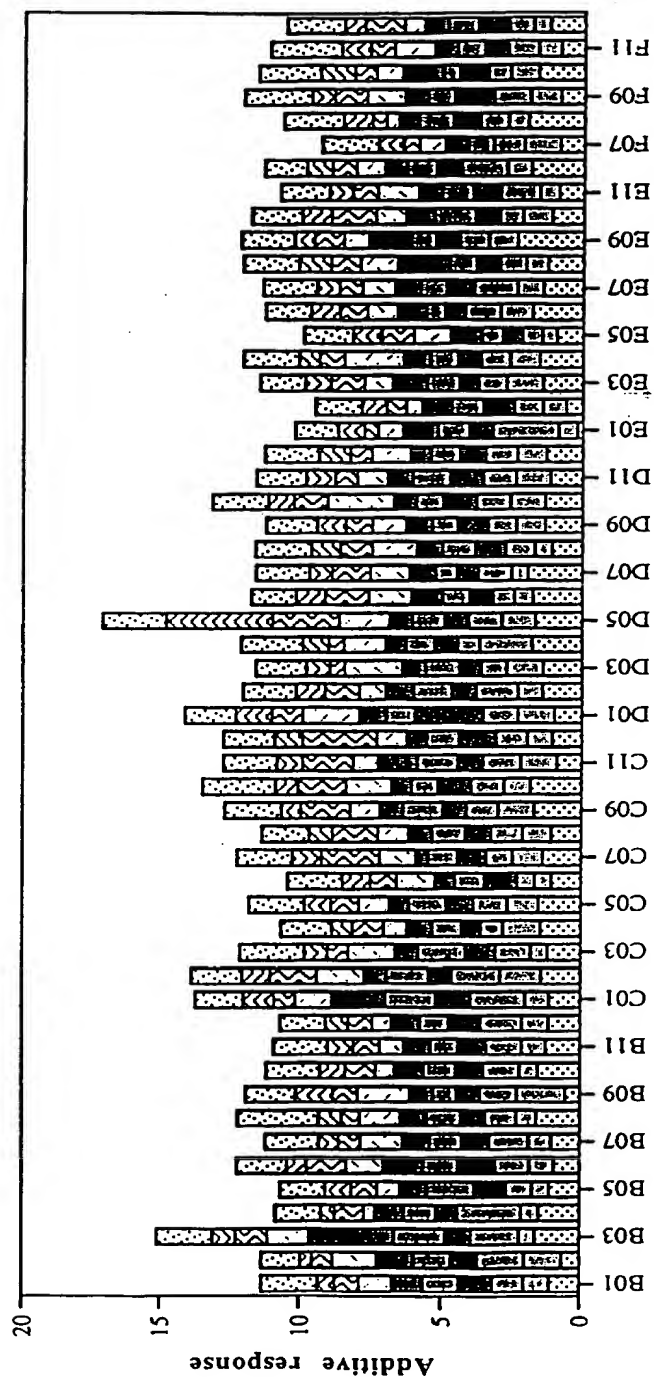


FIG. 5

1	A12	IKDFHVFYFRESRDAG	49	E12	SATSRGVLVVAASGN
2	A11	LEQAVNSATSRGVLV	50	E11	SRGVLVVAASGN SGA
3	A10	AQSVPWGISRVQAPA	51	E10	VLVVAASGN SGA GSI
4	A9	VPWGISRVQAPAAHN	52	E9	VAASGN SGA GSI SYP
5	A8	GISRVQAPAAHNRGL	53	E8	SGNSGA GSI SYPARY
6	A7	RVQAPAAHNRGLTGS	54	E7	SGAGSI SYPARYANA
7	A6	APAAHNRGLTGS GVK	55	E6	GSISYPARYANAMAV
8	A5	AHNRGLTGS GVKVAV	56	E5	SYPARYANAMAVGAT
9	A4	RGLTGS GVKVAVLDT	57	E4	ARYANAMAVGATDQN
10	A3	TGS GVKVAVLDTGIS	58	E3	ANAMAVGATDQNNNR
11	A2	GVKVAVLDTGISTHP	59	E2	MAVGATDQNNNRASF
12	A1	VAVLDTGISTHPDLN	60	E1	GATDQNNNRASF SQY
13	R12	LDTGISTHPDLNIRG	61	F12	DQNNNRASF SQY GAG
14	B11	GISTHPDLNIRGGAS	62	F11	NNRASFSQY GAGLDI
15	B10	THPDLNIRGGAS FVP	63	F10	ASF SQY GAGLDIVAP
16	B9	DLNIRGGAS FVP GEP	64	F9	SQY GAGLDIVAPGVN
17	B8	IRGGAS FVP GEPSTQ	65	F8	GAGLDIVAPGVNVQS
18	B7	GAS FVP GEPSTQDGN	66	F7	LDIVAPGVNVQSTYP
19	B6	FVP GEPSTQDGN GHG	67	F6	VAPGVNVQSTYP GST
20	B5	GEPSTQDGN GHGTHV	68	F5	GVNVQSTYP GSTYAS
21	B4	STQDGN GHGTHVAGT	69	F4	VQSTYP GSTYASLNG
22	B3	DGN GHGTHVAGTIAA	70	F3	TYP GSTYASLNGTSM
23	B2	GHGTHVAGTIAALNN	71	F2	GSTYASLNGTSMATP
24	B1	THVAGTIAALNNSIG	72	F1	YASLNGTSMATPHVA
25	C12	AGTIAALNNSIGVLG	73	G12	LNGTSMATPHVAGAA
26	C11	IAALNNSIGVLGVAP	74	G11	TSMATPHVAGAAALV
27	C10	LNNSIGVLGVAPSAE	75	G10	ATPHVAGAAALVKQK
28	C9	SIGVLGVAPSAELYA	76	G9	HVAGAAALVKQKNPS
29	C8	VLGVAPSAELYAVKV	77	G8	GAAALVKQKNPSWSN
30	C7	VAPSAELYAVKVLGA	78	G7	ALVKQKNPSWSNVQI
31	C6	SAELYAVKVLGASGS	79	G6	KQKNPSWSNVQIRNH
32	C5	LYAVKVLGASGSGSV	80	G5	NPSWSNVQIRNHLKN
33	C4	VKVLGASGSGSVSSI	81	G4	WSNVQIRNHLKNTAT
34	C3	LGASGSGSVSSIAQG	82	G3	VQIRNHLKNTATSLG
35	C2	SGSGSVSSIAQGLEW	83	G2	RNHLKNTATSLGSTN
36	C1	GSVSSIAQGLEWAGN	84	G1	LKNTATSLGSTNLYG
37	D12	SSIAQGLEWAGNNGM	85	H12	TATSLGSTNLYG SGL
38	D11	AQGLEWAGNNGMHVA	86	H11	SLGSTNLYG SGLVNA
39	D10	LEWAGNNGMHVANLS	87	H10	STNLYG SGLVNAEAA
40	D9	AGNNGMHVANLSLGS	88	H9	NLYG SGLVNAEAA TR
41	D8	NGMHVANLSLGS PPS			
42	D7	HVANLSLGS PPS SAT			
43	D6	NLSLGS PPS SATLEQ			
44	D5	LGSPSPSATLEQAVN			
45	D4	PSPSATLEQAVNSAT			
46	D3	SATLEQAVNSATSRG			
47	D2	LEQAVNSATSRGVLV			
48	D1	AVNSATSRGVLVVA			

FIG. 6A

1	A12	IKDFHVYFRESRDAG	49	E12	KKIDVLNLSIGGPDF
2	A11	DAELHIFRVFTNNQV	50	E11	DVLNLSIGGPDFMDH
3	A10	PLRRASLSLGSFVWH	51	E10	NLSIGGPDFMDHPFV
4	A9	RASLSLGSFVWHATG	52	E9	IGGPDFMDHPFVDKV
5	A8	LSLGSFVWHATGRHS	53	E8	PDFMDHPFVDKVVWEL
6	A7	GSFVWHATGRHSSRR	54	E7	MDHPFVDKVVWELTAN
7	A6	FVWHATGRHSSRLLR	55	E6	PFVDKVVWELTANNVI
8	A5	ATGRHSSRLLRAIP	56	E5	DKVVWELTANNVIMVS
9	A4	RHSSRLLRAIPRQV	57	E4	WELTANNVIMVSAIG
10	A3	SRLLRAIPRQVAQT	58	E3	TANNVIMVSAIGNDG
11	A2	LLRAIPRQVAQTLQA	59	E2	NVIMVSAIGNDGPLY
12	A1	AIPRQVAQTLQADV	60	E1	MVSAIGNDGPLYGTJ
13	B12	RQVAQTLQADVWQM	61	F12	AIGNDGPLYGTLLNNP
14	B11	AQTLQADVWQMGYT	62	F11	NDGPLYGTLLNNPADQ
15	B10	LQADVWQMGYTGAN	63	F10	PLYGTLLNNPADQMDV
16	B9	DVLWQMGYTGANVRV	64	F9	GTLLNNPADQMDVIGV
17	B8	WQMGYTGANVRVAVF	65	F8	NNPADQMDVIGVGGI
18	B7	GYTGANVRVAVFDTG	66	F7	ADQMDVIGVGGIDFE
19	B6	GANVRVAVFDTGLSE	67	F6	MDVIGVGGIDFEDNI
20	B5	VRVAVFDTGLSEKHP	68	F5	IGVGGIDFEDNIARF
21	B4	AVFDTGLSEKHPHFK	69	F4	GGIDFEDNIARFSSR
22	B3	DTGLSEKHPHFKNVK	70	F3	DFEDNIARFSSRGMT
23	B2	LSEKHPHFKNVKERT	71	F2	DNIARFSSRGMTTWE
24	B1	KHPHFKNVKERTNWT	72	F1	ARFSSRGMTTWELPG
25	C12	HFKNVKERTNWTNER	73	G12	SSRGMTTWELPGGYG
26	C11	NVKERTNWTNERTLD	74	G11	GMTTWELPGGYGRMK
27	C10	ERTNWTNERTLDDGL	75	G10	TWELPGGYGRMKPDI
28	C9	NWTNERTLDDGLGHG	76	G9	LPGGYGRMKPDIVTY
29	C8	NERTLDDGLGHGTFV	77	G8	GYGRMKPDIVTYGAG
30	C7	TLDDGLGHGTFVAGV	78	G7	RMKPDIVTYGAGVRG
31	C6	DGLGHGTFVAGVIAS	79	G6	PDIVTYGAGVRGSGV
32	C5	GHGTFVAGVIASMRE	80	G5	VTYAGVRGSGVKGG
33	C4	TFVAGVIASMRECQG	81	G4	GAGVRGSGVKGGCRA
34	C3	AGVIASMRECQGFAP	82	G3	VRGSGVKGGCRALSG
35	C2	IASMRECQGFAPDAE	83	G2	SGVKGGCRALSGTSV
36	C1	MRECQGFAPDAELHI	84	G1	KGGCRALSGTSVASP
37	D12	CQGFAPDAELHIFRV	85	H12	CRALSGTSVASPVVA
38	D11	FAPDAELHIFRVFTN	86	H11	LSGTSVASPVVAGAV
39	D10	DAELHIFRVFTNNQV	87	H10	TSVASPVVAGAVTLL
40	D9	LHIFRVFTNNQVSYT	88	H9	ASPVVAGAVTLLVST
41	D8	FRVFTNNQVSYTSWF	89	H8	VVAGAVTLLVSTVQK
42	D7	FTNNQVSYTSWFLDA	90	H7	GAVTLLVSTVQKREL
43	D6	NQVSYTSWFLDAFNY	91	H6	TLLVSTVQKRELVPN
44	D5	SYTSWFLDAFNYAIL	92	H5	VSTVQKRELVPNASM
45	D4	SWFLDAFNYAILKKI	93	H4	VQKRELVPNASMKQA
46	D3	LDAFNYAILKKIDVL	94	H3	RELVPNASMKQALIA
47	D2	FNYAILKKIDVLNLS	95	H2	VNPASMKQALIASAR
48	D1	AILKKIDVLNLSIGG	96	H1	ASMKQALIASARRLP

FIG. 6B

97	I12	IKDFHVYFRESRDAG
98	I11	DAELHIFRVFTNNQV
99	I10	KQALIASARRLPGVN
100	I9	LIASARRLPGVNMFE
101	I8	SARRLPGVNMFEQGH
102	I7	RLPGVNMFEQGHGKL
103	I6	GVNMFEQGHGKLDLL
104	I5	MFEQGHGKLDLLRAY
105	I4	QGHGKLDLLRAYQIL
106	I3	GKLDLLRAYQILNSY
107	I2	DLLRAYQILNSYKPQ
108	I1	RAYQILNSYKPQASL
109	J12	QILNSYKPQASLSPS
110	J11	NSYKPQASLSPSYID
111	J10	KPQASLSPSYIDLTE
112	J9	ASLSPSYIDLTECPY
113	J8	SPSYIDLTECPYMWP
114	J7	YIDLTECPYMWPYCS
115	J6	LTECPYMWPYCSQPI
116	J5	CPYMWPYCSQPIYYG

FIG. 6C

MKLVNIWLLLLLVLLCGKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEY EYIVAFNGYFT
 AKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSEFEVIQI KEKQKAGLLTLEDHPNIKRVT PQR
 KVFRSLKYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLR AIPRQVAQ
 TLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGVI ASM
 RECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFN YAILKKIDVLNLSIGGPDFMDHPFVDK VWEL
 TANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMTTWELPGGYGRMKPD
 IVTYGAGVRGSGVKGGCRALSGTSVASPVVAGAVTLLVSTVQKREL VNPASMKQALIASARRLP G
 VNMFEQGHGKLDLLRAYQIILNSYKPQASLSPSYIDLTECPYMWPYCSQPIYYGGMPTV VNVITILN
 GMGVTGRIVDKPDWQPYLPQNGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHVMI
 TVASPAETESKNGAEQTSTVKLPKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPL
 DWNGDHIHTNFRDMYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRRD VD
 NGLSLVIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFSDGLYEGETL
 ANHDMYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAE GGGRIVLYG
 DSNCLDDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVTPERMEGNHLHRYSK
 VLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKVVL PNFRRSNRPQVRPL
 SPGESGAWDIPGGIMPGRYNQEVGQTI PVFAFLGAMVVLAFFVVQINKAKSRPKRRKPRVKRPQL
 MQQVHPPKTPSV

FIG. 7

002200 "E222250

FIG. 8

000001 243250

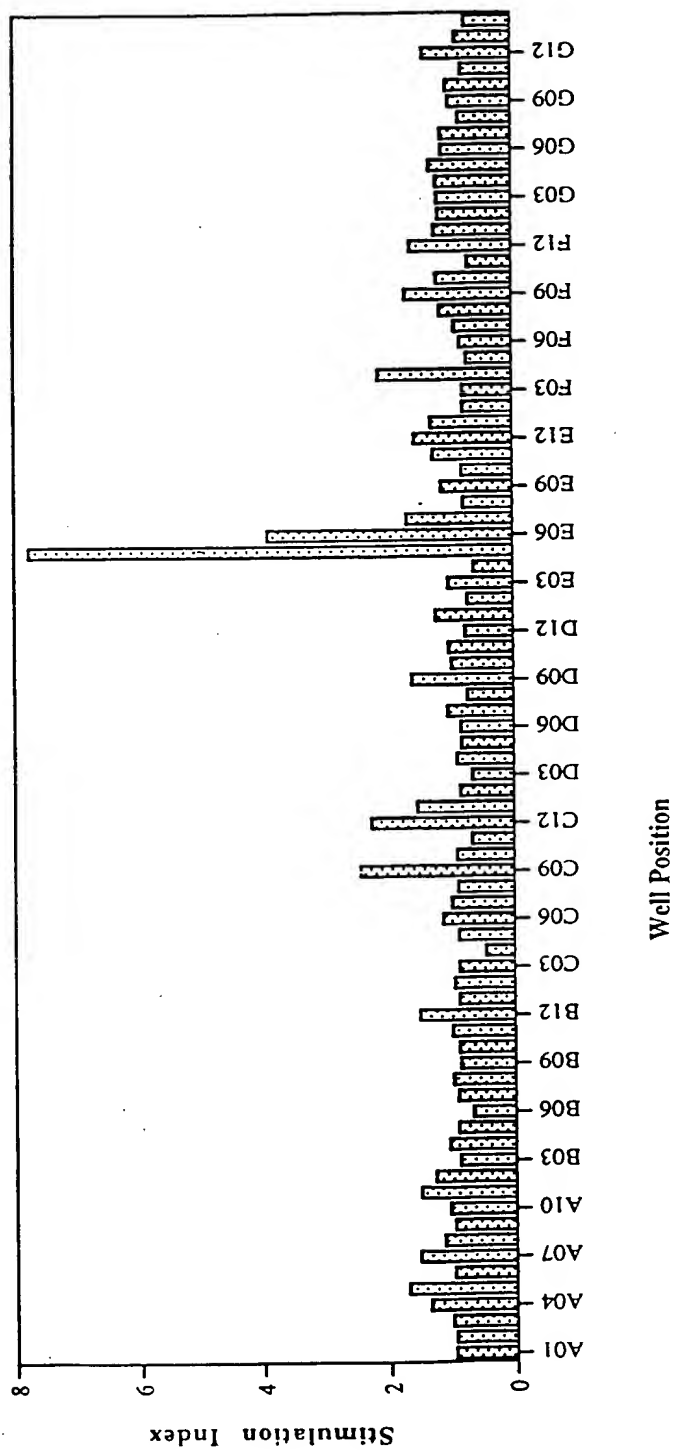


FIG. 9

002007-03-23 14:23:53

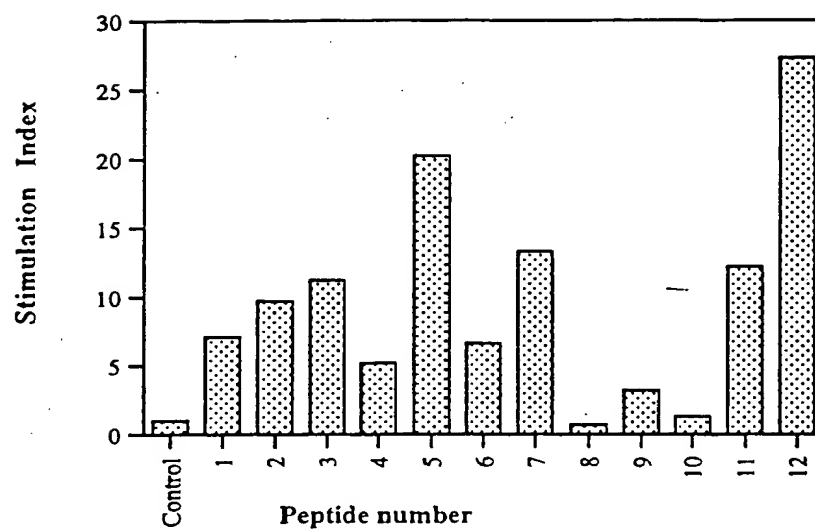
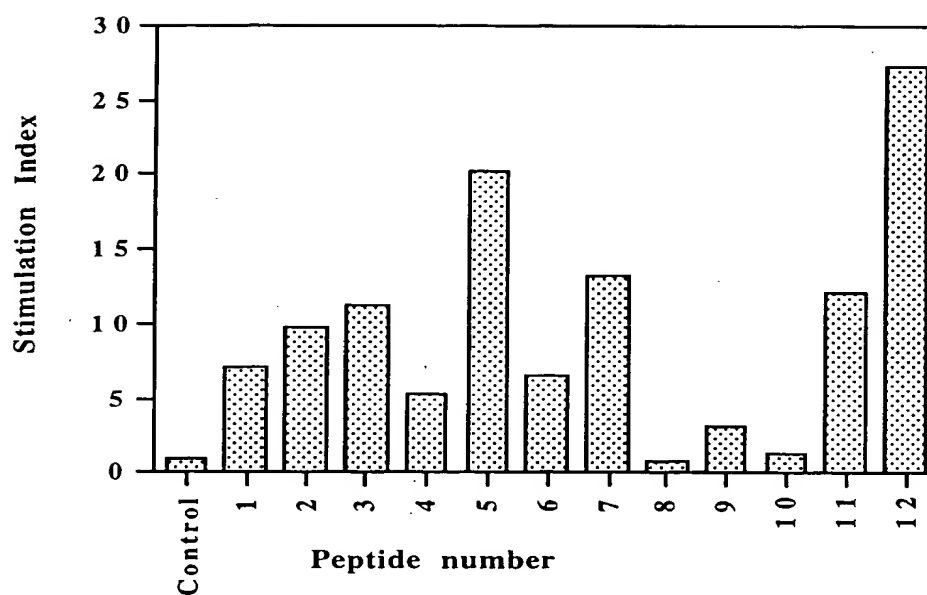


FIG. 10



Peptide number	Sequence
1 (unmodified sequence)	GSISYPARYANAMAV
2	ASISYPARYANAMAV
3	GAISYPARYANAMAV
4	GSASYPARYANAMAV
5	GSIAYPARYANAMAV
6	GSISAPARYANAMAV
7	GSISYAARYANAMAV
8	GSISYPAAAYANAMAV
9	GSISYPARAANAMAV
10	GSISYPARYAAAMAV
11	GSISYPARYANAAAV
12	GSISYPARYANAMAA

FIG. 11

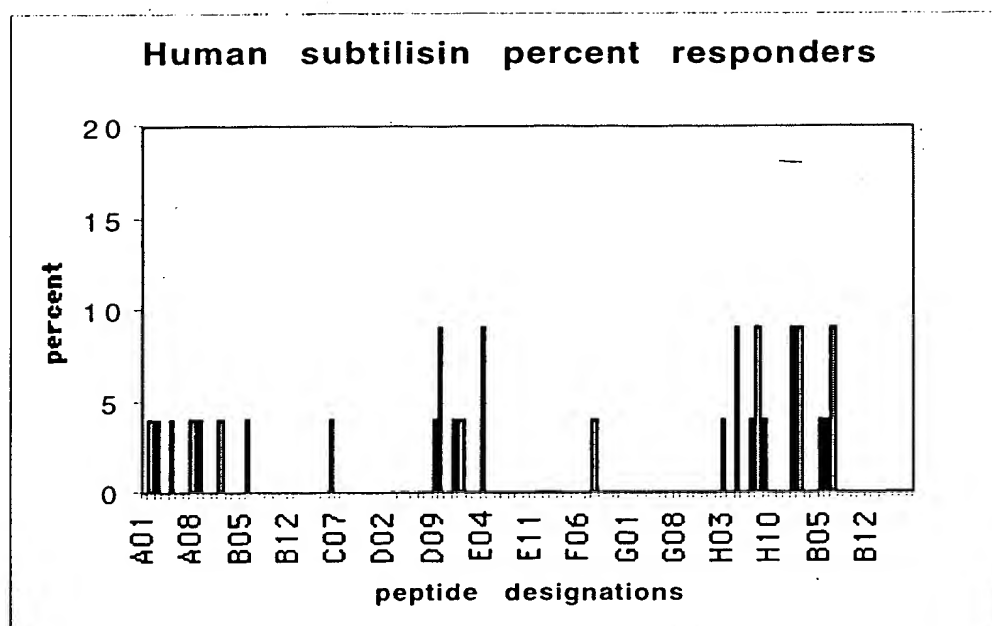


FIG. 12

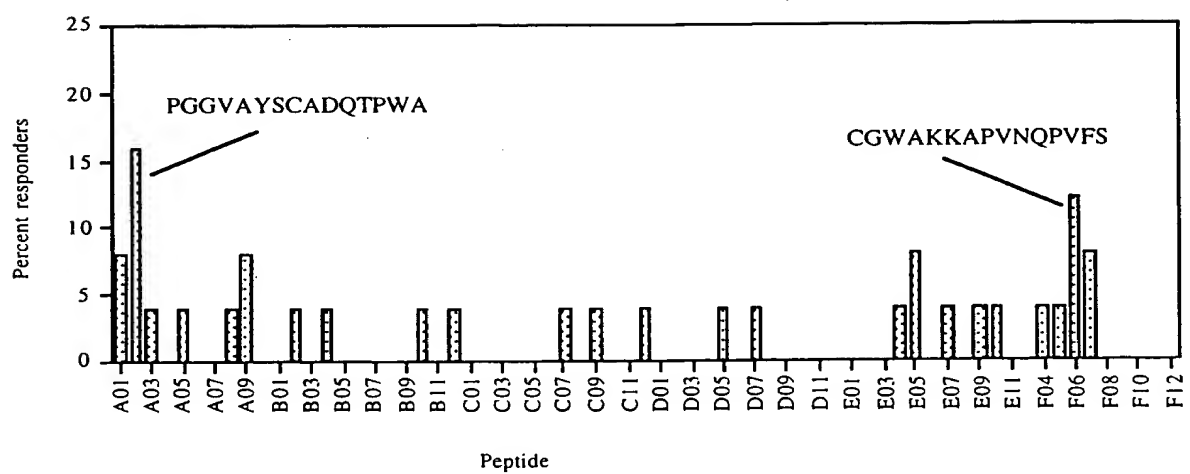


FIG. 13A

1	2	3	4	5
1234567890	1234567890	1234567890	1234567890	1234567890
MRSSPLLPSA	VVAALPVLAL	AADGRSTRYW	DCCKPSCGWA	<u>KKAPVNQPVF</u>
<u>SCNANFQRIT</u>	<u>DFDAKSGCEP</u>	<u>GGVAYSCADQ</u>	<u>TPWAVNDDFA</u>	LGFAATSIAG
SNEAGWCCAC	YELTFTSGPV	AGKKMVVQST	STGGDLGSNH	FDLNIPGGGV
GIFDGCTPQF	GGLPGQRYGC	ISSRNECDRF	PDALKPGCIYW	RFDWFKNADN
PSFSFRQVQC	PAELVARTGC	RRNDDGNFPA	VQIPSSSTSS	PVNQPTSTST
TSTSTTSSPP	VQPTTPSGCT	AERWAQ		

FIG. 13B

GDVTGFLALDNTNKLIVL

SIENWIGNLNF DLKE

percent on 25

A01 A04 A07 A10 B03 B06 B09 B12 C03 C06 C09 C12 D03 D06 D09 D12 E03 E06 E09 E12 F03 F06 F09 F12 G03 G06 G09 G12 H11

Column I

THESE PEPTIDES ARE CONSECUTIVE

FIG. 14A

002004 " 228/2980

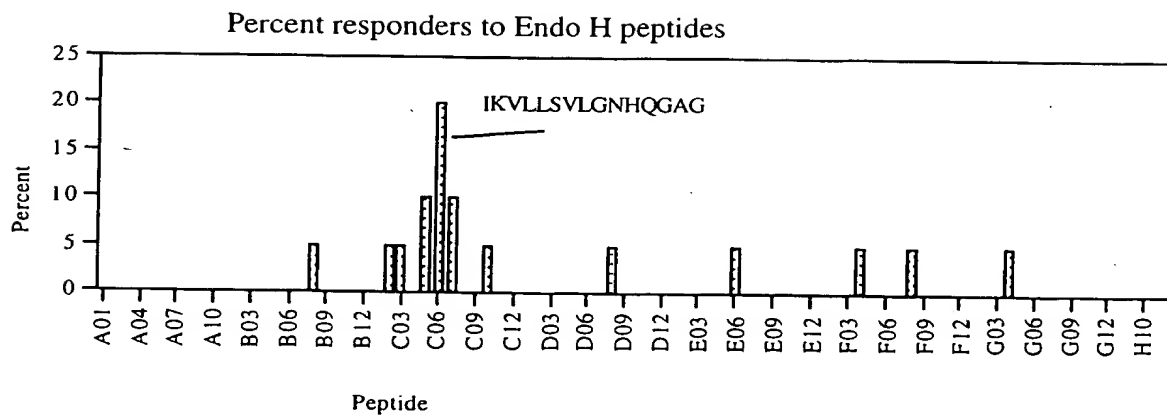


FIG. 15A

006780 000000

1 mftpvrrrvr taalalsaaa alvlgstaas gasatpspap apapapvkqg
51 ptsvayvevn nnsmlnvgy tladgggnaf dvavifaani nydtgktay
101 lhfenvqrv ldnavtqirp lqqqgikvll svlqnhggag fanfpsqqaa
151 safakqlsda vakygldgvd fddeyaeygn ngtagpndss fvhlvtalra
201 nmpdkiisly nigpaasrls yggvdvskf dyawnpyygt wqvpqialpk
251 aqlspaavei grtsrstvad larrtvdegy gvyltynldg gdrtdavsaf
301 trelygseav rtp

FIG. 15B

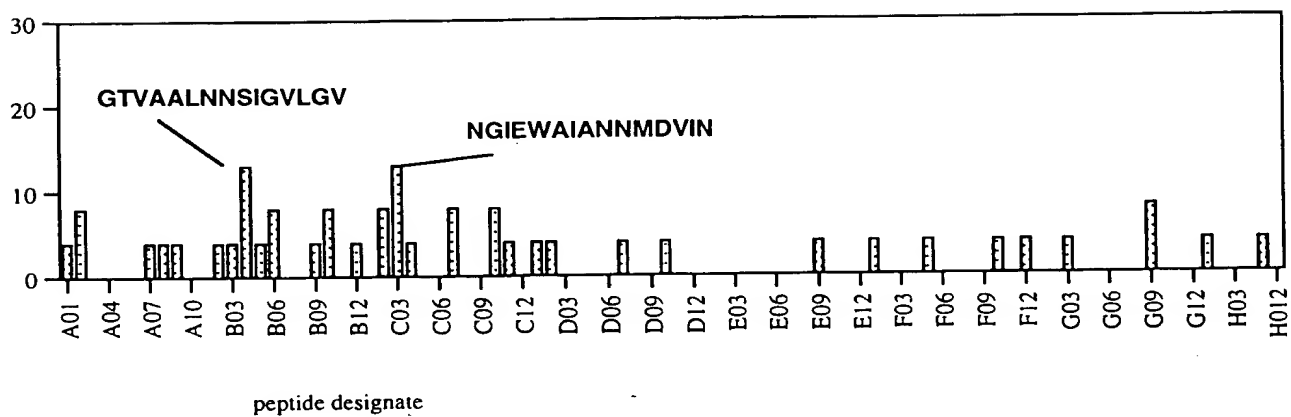


FIG. 16

2007-06-22 10:00

GG36 percent responders

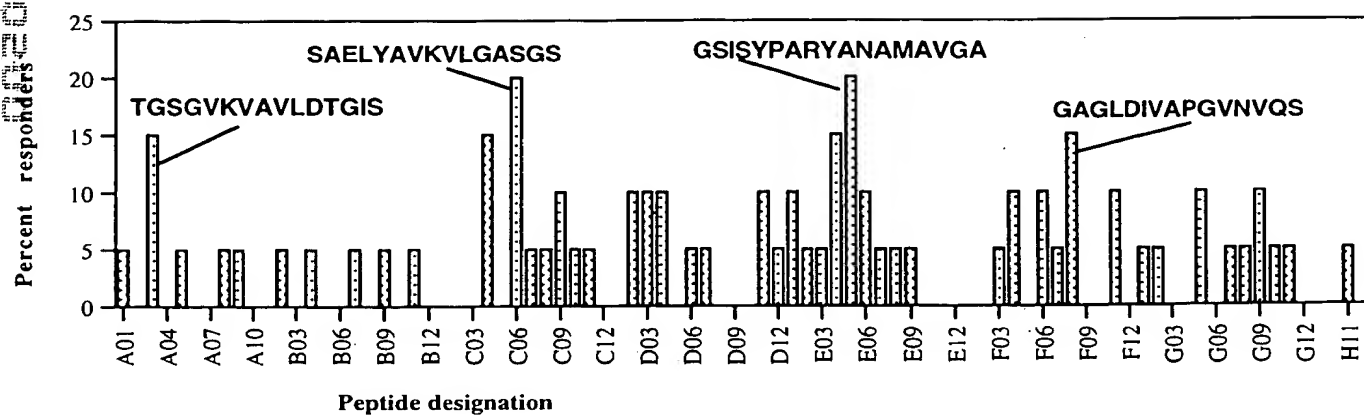


FIG. 17

Hybrid enzyme sequence (GG36-BPN)

GG36

AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPTQDGNGH

BPN

GTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVINMSLGGS

Δ

GSAALKAAVDKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGP

ELDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGD

SFYY GKGLINVQAAAQ

FIG. 18

002007" 2002/2960

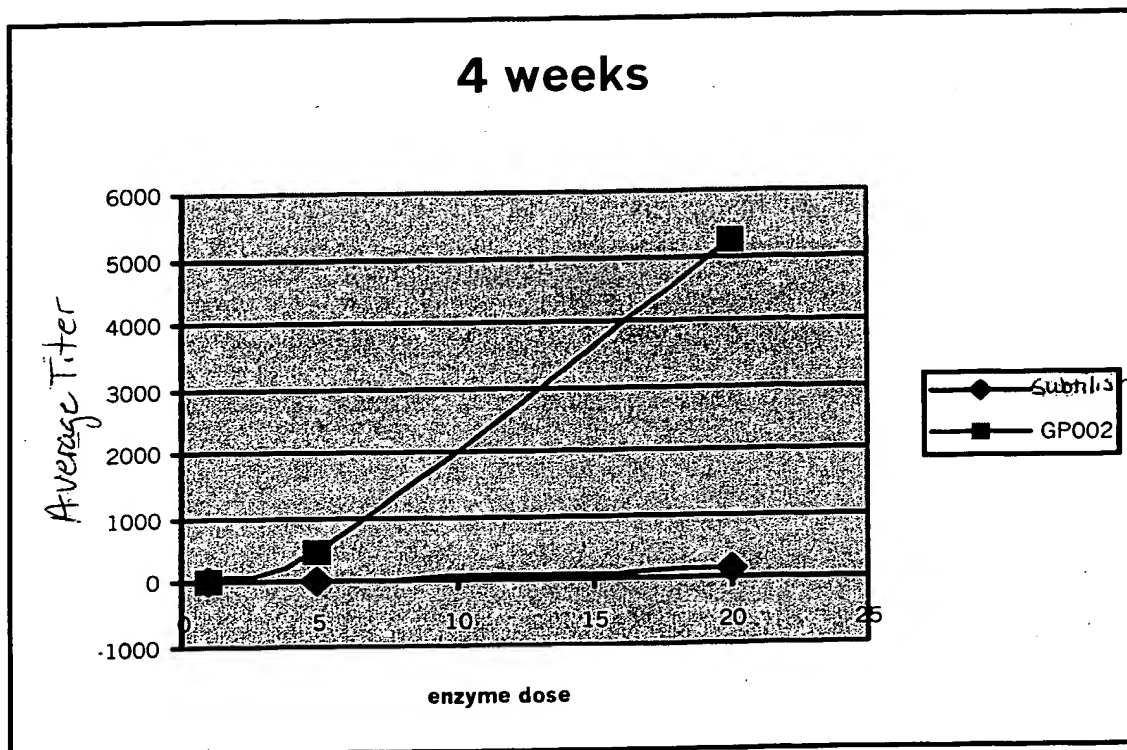


FIGURE 19A

09677822 100000

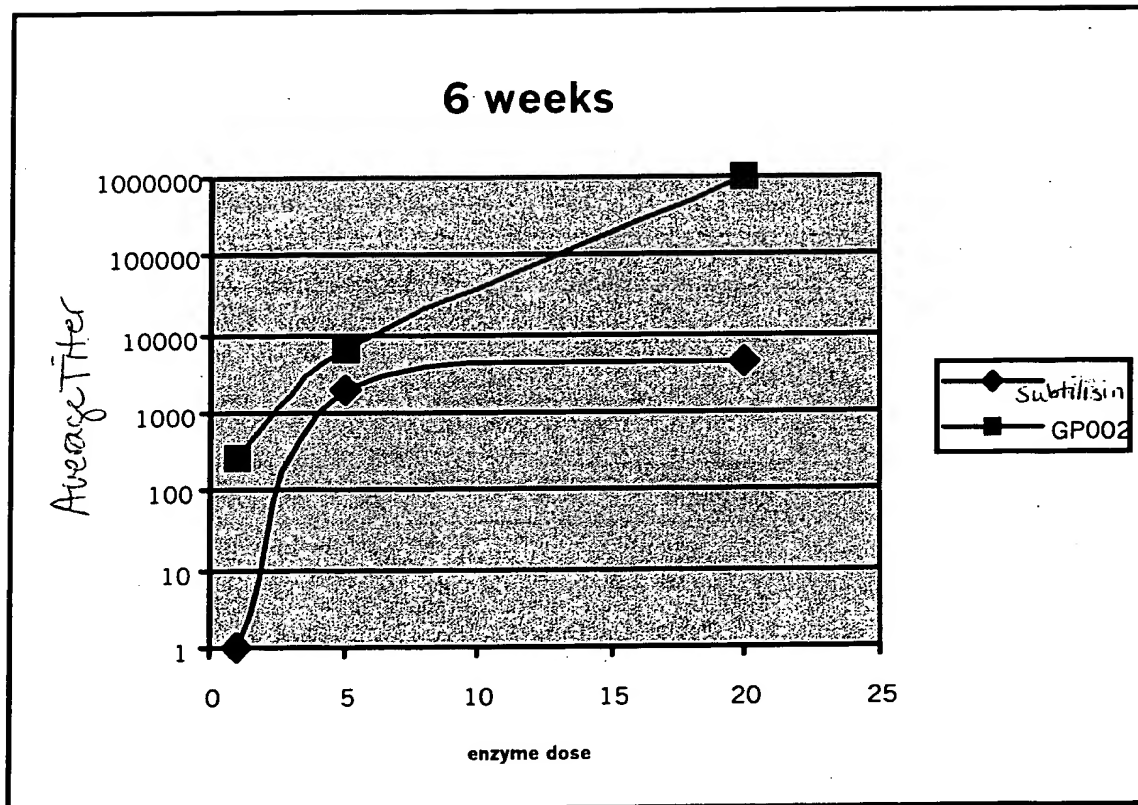


FIGURE 19B

09677833 100200

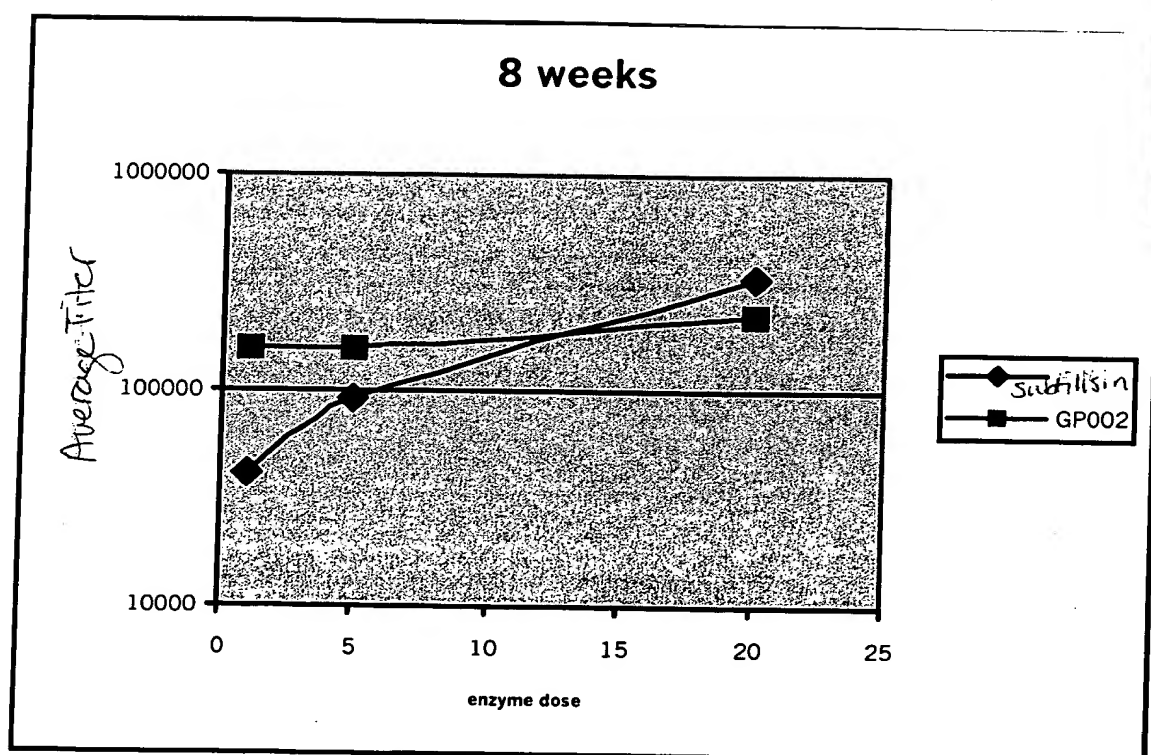


FIGURE 19C

000001 22844960

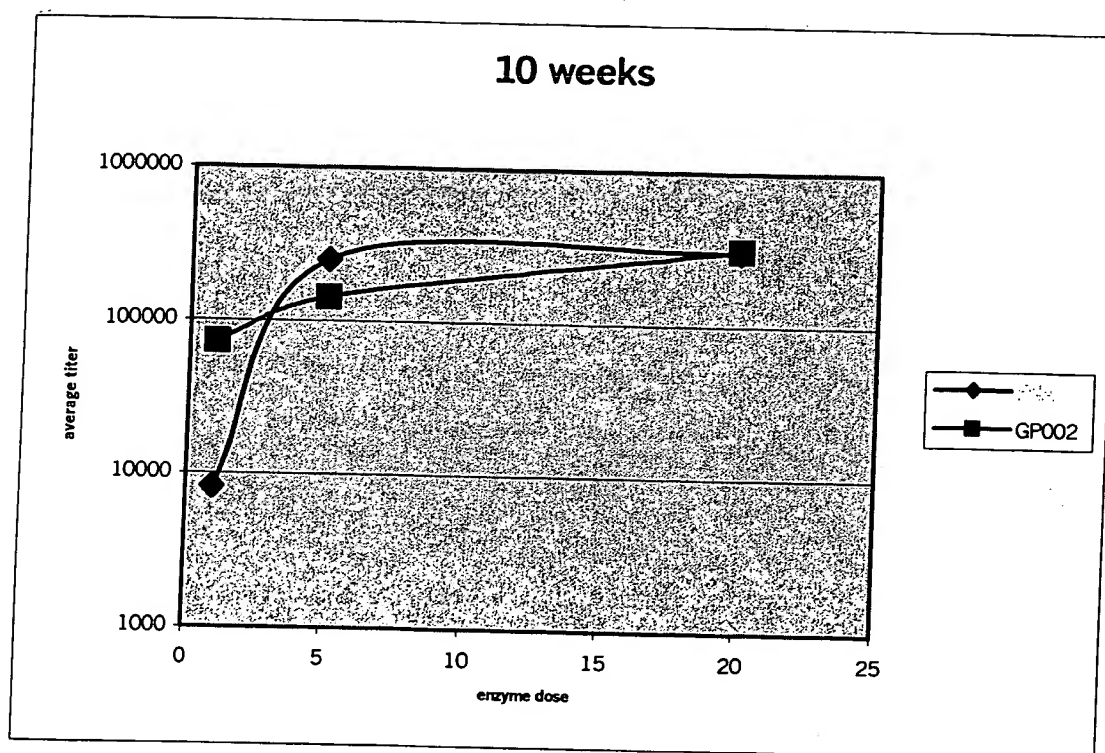


FIGURE 19D

000007 29822950

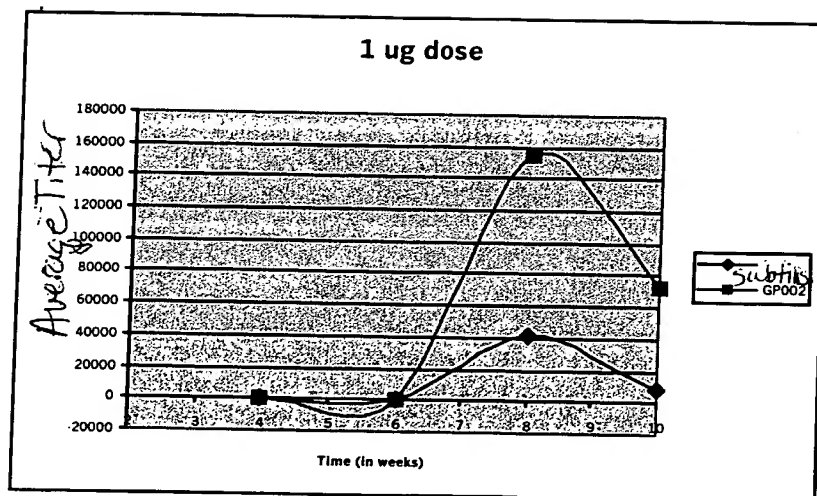


FIGURE 20A

002007 2252560

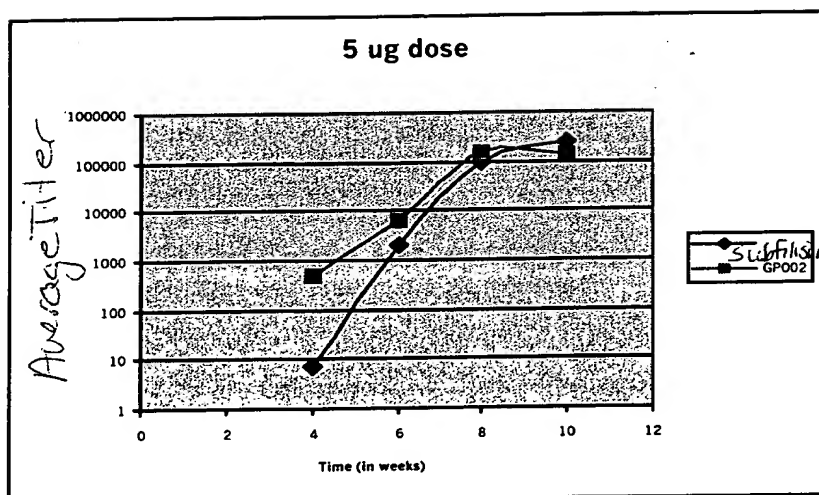


FIGURE 20B

002007 22042960

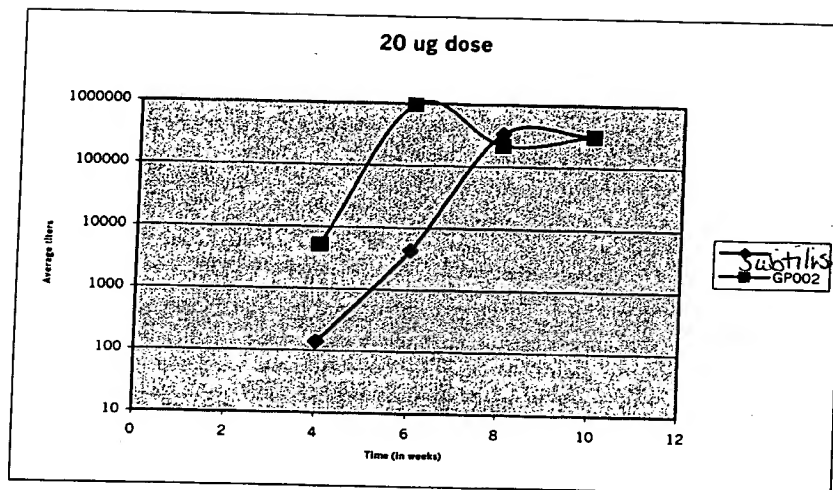


FIGURE 20C